Amendment and Listing of the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-52. (cancelled)

Claim 53. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed in soybean, produces an RNA having:

(a) homology to at least one target mRNA expressed in soybean, and

(b) two fully complementary RNA regions which are unrelated to any endogenous RNA in the host and which are transcribed from SEQ ID NO:13 , comprising at least nucleotides 7-36 and 82-111 or 7-36, 44-73, 82-111 and 119-148 of SEQ ID NO: 13, and which are in proximity operably linked to a sequence homologous to all or part of the target mRNA in (a), wherein the recombinant construct, when expressed in soybean reduces expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the target mRNA in (a) based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 54. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed in soybean, produces an RNA having:

(a) homology to at least one target mRNA expressed in soybean,

(b) an RNA region which is unrelated to any endogenous RNA in the host and which is transcribed from SEQ ID NO:13, comprising at least nucleotides 7-36 or 7-36 and 44-73 of SEQ ID NO: 13 and is located 5' to a sequence homologous to all or part of the target mRNA in (a), and

(c) the reverse complement of (b), comprising at least nucleotides 82-111 or 82-111 and 119-148 of SEQ ID NO: 13 and is located 3' to a sequence homologous to all or part of the target mRNA in (a), further wherein the recombinant construct expressed by the host reduces the expression of the target mRNA or any

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endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the target mRNA described in (a) based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 55. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed in soybean, produces an RNA having:

(a) homology to at least one target mRNA expressed in soybean, and

(b) two fully complementary RNA regions, which are unrelated to any endogenous RNA in soybean, which are transcribed from SEQ ID NO:13, said SEQ ID NO:13 comprising a NotI site, and which are in proximity operably linked to a sequence homologous to all or part of the target mRNA in (a), wherein said a DNA sequence that has at least 80% sequence identity with all or a part of a target DNA in soybean homologous is introduced into the NotI site of SEQ ID NO:13 and wherein the recombinant construct, when expressed in soybean reduces expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the target RNA in a) based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 56. (currently amended) A method for reducing expression of a target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of a RNA homologous to a target mRNA expressed in soybean based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, the method comprising:

(a) transforming soybean with any of the recombinant constructs of Claims 46-47 53-55; and

(b) selecting soybean which have reduced expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with a sequence homologous to all or part of the RNA homologous to the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, said reduction in expression being determined by comparison with the level of expression in an untransformed soybean.

Claim 57. (currently amended) An RNA comprising:

(a) homology to at least one target mRNA expressed in soybean, and

(b) two fully complementary RNA regions ~~, which are unrelated to any endogenous RNA in soybean and~~ which are transcribed from SEQ ID NO:13 , comprising at least nucleotides 7-36 and 82-111 or 7-36, 44-73, 82-111 and 119-148 of SEQ ID NO: 13, and which are ~~in proximity~~ operably linked to a sequence homologous to all or part of the target mRNA in (a), wherein the RNA ~~in (a) and (b)~~, when introduced into soybean, reduces expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with the sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 58. (currently amended) An RNA comprising:

(a) homology to at least one target mRNA expressed in soybean,

(b) an RNA region ~~, which is unrelated to any endogenous RNA in soybean and~~ which is transcribed from SEQ ID NO:13, comprising at least nucleotides 7-36 or 7-36 and 44-73 of SEQ ID NO:13 and is located 5' to a sequence homologous to all or part of the target mRNA in (a), and

(c) the reverse complement of (b), comprising at least nucleotides 82-111 or 82-111 and 119-148 of SEQ ID NO:13 and located 3' to a sequence homologous to all or part of the target mRNA in (a), wherein the RNA ~~in (a) and (b)~~ , when introduced into the host, reduces the expression of the target mRNA or any endogenous mRNA that has at least 80% sequence identity with the sequence homologous to all or part of the target mRNA based on the Clustal method of

alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4.

Claim 59. (previously presented) A method for reducing expression in soybean of a target mRNA or any endogenous mRNA having at least 80% sequence identity with a sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4, the method comprising:

(a) introducing into soybean any of the RNA of Claims 57or 58; and

(b) selecting soybeans which have reduced expression of the target mRNA or any endogenous mRNA having at least 80% sequence identity with the sequence homologous to all or part of the target mRNA based on the Clustal method of alignment wherein the default parameters for multiple alignment of the sequences are GAP PENALTY=10, GAP LENGTH PENALTY=10 and for pairwise alignments KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4 , said reduction in expression being determined by comparison with the level of expression in an untransformed soybean.